

**Figure 1: 108P5H8 SSH sequence of 448 nucleotides (SEQ ID: 2568)**

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1 GATCCAGATT TCTCTGCACA CTGGACTTCG TAGAGTAAGT GTGGTAGACA AAGAGACTAC
61 ACTGCACAAC CACCAGTGAA TATCATTGCT AAGAAGACTT TGGGTCGTGT TTCTCAGCCA
121 CTCTCACAGC TTTTGTAGAC TTATTTGATT TTGAAACAAG CAGTTAGCTA AATCTATTTT
181 CCTTTTATGC ATATATGTTA ATTGGCTCAA CTTAATATGG TGTTCTTACA GAATATGAGC
241 CCATTTGAAA TAAGGTTTTA GGCAATTTTG CTGTTGGCTC TGATTTGTAT ATAGCAAATT
301 TAAAGGTACA GAGTGTTCCT TAGATAGAAG ATTAGTTCAT TTGGTTCATT TTGTCTTTGA
361 AGCAAGCCAA GCTCATGAGC CAGTTGGTTA TTTGTCATAA ATGAACACCC ATCACTATAT
421 GCTATGTTGA GGGGAGGCAA GGCTGATC

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**Figure 2A. The cDNA (SEQ ID. NO. :2569) and amino acid sequence (SEQ ID. NO. :2570) of 108P5H8 v.1. The start methionine is underlined. The open reading frame extends from nucleic acid 253-1542 including the stop codon.**

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1 gccggcctccagcagcgggcgcggcgggcgagcagacccactctcctgcggccgcg
61 ggtggagcagcgcgagcccgccctcgctgagccggcgggggcgaggagatgagttgcggc
121 cccgcggcagcgcgccccaggatggggaggagcgcgcggcactgccctcgagaactggcgct
181 ccggtgaagtaggcgcgcggccgctccgcctcccccaagccgttcgcaccgcggccgcg
1      M A G S G A W K R L K S M L R K
241 tcagcctctgccATGGCCGGCTCTGGCGCTGGAAGCGCCTCAAATCTATGCTAAGGAAG
17 D D A P L F L N D T S A F D F S D E A G
301 GATGATGCGCCGCTGTTTTTAAATGACACCAGCGCCTTTGACTTCTCGGATGAGGCGGGG
37 D E G L S R F N K L R V V V A D D G S E
361 GACGAGGGGCTTTCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAA
57 A P E R P V N G A H P T L Q A D D D S L
421 GCCCCGGAAGGCCTGTTAACGGGGCGCACCCGACCCTCCAGGCCGACGATGATTCCTTA
77 L D Q D L P L T N S Q L S L K V D S C D
481 CTGGACCAAGACTTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGAC
97 N C S K Q R E I L K Q R K V K A R L T I
541 AACTGCAGCAAACAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATT
117 A A V L Y L L F M I G E L V G G Y I A N
601 GCTGCCGTTCTGTACTTGCTTTTCATGATTGGAGAACTGTAGGTGGATACATTGCAAAT
137 S L A I M T D A L H M L T D L S A I I L
661 AGCCTAGCAATCATGACAGATGCACTTCATATGTAACTGACCTAAGCGCCATCATACTC
157 T L L A L W L S S K S P T K R F T F G F
721 ACCCTGCTTGCTTTGTGGCTATCATCAAAATCACCAACCAAAGATTACCTTTGGATTT
177 H R L E V L S A M I S V L L V Y I L M G

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781 CATCGCTTAGAGGTTTTGTCAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGA  
197 F L L Y E A V Q R T I H M N Y E I N G D  
841 TTCCTCTTATATGAAGCTGTGCAAAGAACTATCCATATGAACATGAAATAAATGGAGAT  
217 I M L I T A A V G V A V N V I M G F L L  
901 ATAATGCTCATCACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTG  
237 N Q S G H R H S H S H S L P S N S P T R  
961 AACCAGTCTGGTCACCGTCACTCCCATTTCCCACTCCCTGCCTTCAAATTTCCCCTACCAGA  
257 G S G C E R N H G Q D S L A V R A A F V  
1021 GGTTCCTGGGTGTGAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTTGTGTA  
277 H A L G D L V Q S V G V L I A A Y I I R  
1081 CATGCTTTGGGAGATTGTTGACAGAGTGTGTTGGTGTGCTAATAGCTGCATACATCATACGA  
297 F K P E Y K I A D P I C T Y V F S L L V  
1141 TTCAAGCCAGAATACAAGATTGCTGACCCCATCTGTACATACGTATTTTCATTACTTGTG  
317 A F T T F R I I W D T V V I I L E G V P  
1201 GCTTTTACAACATTTTGAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCA  
337 S H L N V D Y I K E A L M K I E D V Y S  
1261 AGCCATTTGAATGTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCA  
357 V E D L N I W S L T S G K S T A I V H I  
1321 GTCGAAGATTTAAATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATA  
377 Q L I P G S S S K W E E V Q S K A N H L  
1381 CAGCTAATTCCTGGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTTA  
397 L L N T F G M Y R C T I Q L Q S Y R Q E  
1441 TTATTGAACACATTTGGCATGTATAGATGTACTATTTCAGCTTCAGAGTTACAGGCAAGAA  
417 V D R T C A N C Q S S S P \*  
1501 GTGGACAGAACTTGTGCAAATTGTCAGAGTTCCTAGTCCCTAAAttttatgtattttgggaa  
1561 ctcctgccttattttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatga  
1621 gaaaatggaatccctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccc  
1681 cagcctgacagtgctagtctctgttttaattggtaaaaggagactttgccataattttcaga  
1741 tgaagatgtttcccaaactgtttacagaatgagatgtgactctacagatacctcatag  
1801 aagacaatccaagatcatacttcattaacttgacagagtagctgtcttaaaggaagcatc  
1861 aagaattcaatattttgcatttaaaaaatactttttaaggccattttatattaagccagtg  
1921 tggaaaactgaatttttttttattatgtataataatctcgacaccagcttctggaattgc  
1981 tgctttctttttacagaaattactacccaacagatttcaggaagtactagtagttatccc  
2041 aaaagtgggaataagcatgtattcctaagtgtttcagaaatgttttatttcacacataagt  
2101 cttaatgttattgttatgattatactttataaacaaccttttcagatgctacagggttt  
2161 tgaatctcaaagttaacattttttcattatttgaatcttagaaccaaatctttattttatt  
2221 gtggtcactgttattaaatgatttaggaaatactttcaatattattctgaatggctgaag

2281 ttagtctttaaactcaaattactatatgatgattttaaacaataaaagagcgaggatgg

2341 ggaaaaaaaaaaaaaaaaaaaaa

**Figure 2B. The cDNA (SEQ ID. NO. :2571) and amino acid sequence (SEQ ID. NO. :2572) of 108P5H8 v.2.** The start methionine is underlined. The open reading frame extends from nucleic acid 1-1290 including the stop codon.

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1 M A G S G A W K R L K S M L R K D D A P
1 ATGGCCGGCTCTGGCGCGTGGAAGCGCCTCAAATCTATGCTAAGGAAGGATGATGCGCCG
21 L F L N D T S A F D F S D E A G D E G L
61 CTGTTTTTAAATGACACCAGCGCCTTTGACTTCTCGGATGAGGCGGGGACGAGGGGCTT
41 S R F N K L R V V V A D D G S E A P E R
121 TCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAAGCCCCGAAAGG
61 P V N G A H P T L Q A D D D S L L D Q D
181 CCTGTTAACGGGGCGACCCGACCCTCCAGGCCGACGATGATTCTTACTGGACCAAGAC
81 L P L T N S Q L S L K V D S C D N C S K
241 TTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGACAACTGCAGCAAA
101 Q R E I L K Q R K V K A R L T I A A V L
301 CAGAGAGAGATACTGAAGCAGAGAAAAGTGAAAGCCAGGTTGACCATTGCTGCCGTTCTG
121 Y L L F M I G E L V G G Y I A N S L A I
361 TACTTGCTTTTTCATGATTGGAGAAGTTGTAGGTGGATACATTGCAAATAGCCTAGCAATC
141 M T D A L H M L T D L S A I I L T L L A
421 ATGACAGATGCACTTCATATGTAACTGACCTAAGCGCCATCATACTCACCCCTGCTTGCT
161 L W L S S K S P T K R F T F G F H R L E
481 TTGTGGCTATCATCAAATCACCAACCAAAGATTACCTTTGGATTTCATCGCTTAGAG
181 V L S A M I S V L L V Y I L M G F L L Y
541 GTTTTGTGAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGATTCTCTTATAT
201 E A V Q R T I H M N Y E I N G D I M L I
601 GAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGATATAATGCTCATC
221 T A A V G V A V N V I M G F L L N Q S G
661 ACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTGAACCAGTCTGGT
241 H R H S H S H S L P S N S P T R G S G C
721 CACCGTCACTCCCATTCCCCTCCCTGCCTTCAAATTCCCCTACCAGAGGTTCTGGGTGT
261 E R N H G Q D S L A V R A A F V H A L G
781 GAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTTGTACATGCTTTGGGA
281 D L V Q S V G V L I A A Y I I R F K P E
841 GATTTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGATTCAAGCCAGAA
301 Y K I A D P I C T Y V F S L L V A F T T
901 TACAAGATTGCTGATCCCATCTGTACATACGTATTTTTCATTACTTGTGGCTTTTACAACA
321 F R I I W D T V V I I L E G V P S H L N
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961 TTTCTGAATCATATGGGATACAGTAGTTATAATACTAGAAAGGTGTGCCAAGCCATTGAAT  
341 V D Y I K E A L M K I E D V Y S V E D L  
1021 GTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCAGTCGAAGATTTA  
361 N I W S L T S G K S T A I V H I Q L I P  
1081 AATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATACAGCTAATTCCT  
381 G S S S K W E E V Q S K A N H L L L N T  
1141 GGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTATTATTGAACACA  
401 F G M Y R C T I Q L Q S Y R Q E V D R T  
1201 TTTGGCATGTATAGATGTACTATTTCAGCTTCAGAGTTACAGGCAAGAAGTGGACAGAACT  
421 C A N C Q S S S P \*  
1261 TGTGCAAATTGTCAGAGTTCTAGTCCCTAAAttttatgtattttggggactcctgccttat  
1321 ttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatgagaaaatggaatc  
1381 cctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccccagcctgacagt  
1441 gctagtcctctgtttaatggtaaaaggagactttgccataattttcagatgaagatgtttc  
1501 ccaaacactgtttacagaatgagatgtgactctacagatacctcatag

**Figure 2C. The cDNA (SEQ ID. NO. :2573) and amino acid sequence (SEQ ID. NO. :2574) of 108P5H8 v.3. The start methionine is underlined. The open reading frame extends from nucleic acid 1-1290 including the stop codon.**

1 M A G S G A W K R L K S M L R K D D A P  
1 ATGGCCGGCTCTGGCGCGTGGAAGCGCCTCAAATCTATGCTAAGGAAGGATGATGCGCCG  
21 L F L N D T S A F E F S D E A G D E G L  
61 CTGTTTTTAAATGACACCAGCGCCTTTGAGTTCTCGGATGAGGCGGGGACGAGGGGCTT  
41 S R F N K L R V V V A D D G S E A P E R  
121 TCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAAGCCCCGAAAGG  
61 P V N G A H P T L Q A D D D S L L D Q D  
181 CCTGTTAACGGGCGCACCCGACCCTCCAGGCCGACGATGATTCCTTACTGGACCAAGAC  
81 L P L T N S Q L S L K V D S C D N C S K  
241 TTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGACAACTGCAGCAAA  
101 Q R E I L K Q R K V K A R L T I A A V L  
301 CAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATTGCTGCCGTTCTG  
121 Y L L F M I G E L V G G Y I A N S L A I  
361 TACTTGCTTTTCATGATTGGAGAACTTGTAGGTGGATACATTGCAAATAGCCTAGCAATC  
141 M T D A L H M L T D L S A I I L T L L A  
421 ATGACAGATGCACTTCATATGTAACTGACCTAAGCGCCATCATACTCACCCCTGCTTGCT  
161 L W L S S K S P T K R F T F G F H R L E  
481 TTGTGGCTATCATCAAATCACCAACCAAAGATTACCTTTGGATTTCATCGCTTAGAG  
181 V L S A M I S V L L V Y I L M G F L L Y  
541 GTTTTGTGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGATTCCTCTTATAT  
201 E A V Q R T I H M N Y E I N G D I M L I  
601 GAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGATATAATGCTCATC  
221 T A A V G V A V N V I M G F L L N Q S G  
661 ACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTGAACCAGTCTGGT  
241 H R H S H S H S L P S N S P T R G S G C  
721 CACCGTCACTCCCATTCCCCTCCCTGCCTTCAAATCCCCTACCAGAGGTTCTGGGTGT  
261 E R N H G Q D S L A V R A A F V H A L G  
781 GAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTTGTACATGCTTTGGGA  
281 D L V Q S V G V L I A A Y I I R F K P E  
841 GATCTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGATTCAAGCCAGAA  
301 Y K I A D P I C T Y V F S L L V A F T T  
901 TACAAGATTGCTGACCCCATCTGTACATACGTATTTTCATTACTTGTGGCTTTTACAACA

321 F R I I W D T V V I I L E G V P S H L N  
961 TTTCGAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCAAGCCATTTGAAT  
341 V D Y I K E A L M K I E D V Y S V E D L  
1021 GTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCAGTCGAAGATTTA  
361 N I W S L T S G K S T A I V H I Q L I P  
1081 AATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATACAGCTAATTCCT  
381 G S S S K W E E V Q S K A N H L L L N T  
1141 GGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTATTATTGAACACA  
401 F G M Y R C T I Q L Q S Y R Q E V D R T  
1201 TTTGGCATGTATAGATGTACTATTTCAGCTTCAGAGTTACAGGCAAGAAGTGGACAGAACT  
421 C A N C Q S S S P \*  
1261 TGTGCAAATTGTCAGAGTTCTAGTCCCTAAttttatgtattgttttagcattgctgaatt  
1321 cactttatttatcctgcagtcacagacttgagagcaataaatgcaaactaaatgagaaa  
1381 atggaatccctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccccagc  
1441 ctgacagtgcctagtcctctgtttaatggtaaaaggagactttgccataattttcagatgaa  
1501 gatgtttcccaaactgtttacagaatgagatgtgactcctacagatacctcatag

**Figure 3:**

**Figure 3A. Amino acid sequence corresponding to 108P5H8 v.1 (SEQ ID NO: 2570) and 108P5H8 v.2 (SEQ ID. NO. :2572).** The 108P5H8 v.1 and 108P5H8 v.2 proteins have 429 amino acids.

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1  MAGSGAWKRL  KSMRLRKDDAP  LFLNDTSAFD  FSDEAGDEGL  SRFNKL RVVV  ADDGSEAPER
61  PVNGAHPTLQ  ADDDSLDDQD  LPLTNSQLSL  KVDSCDNCSK  QREILKQ RKV  KARLTIAAVL
121 YLLFMIGELV  GGYIANSLAI  MTDALHMLTD  LSAILITLLA  LWLSSKSPTK  RFTFGFHRLE
181 VLSAMISVLL  VYILMGFLLY  EAVQRTIHMN  YEINGDIMLI  TAAVGVA VNV  IMGFLLNQSG
241 HRHSHSHSLP  SNSPTRGSGC  ERNHGQDSL A  VRAAFVHALG  DLVQSVGVLI  AAYIIRFKPE
301 YKIADPICTY  VFSLLVAF TT  FRIIWDTVVI  ILEGVP SHLN  VDYIKEALMK  IEDVYSVEDL
361 NIWSLTSGKS  TAIVHIQLIP  GSSSKWEEVQ  SKANHLLLNT  FGMYRCTIQL  QSYRQEVDR T
421 CANCQSSSP*

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**Figure 3B. Amino acid sequence corresponding to 108P5H8 v.3 (SEQ ID. NO. :2574).**  
The 108P5H8 v.3 protein has 429 amino acids.

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1  MAGSGAWKRL  KSMRLRKDDAP  LFLNDTSAFE  FSDEAGDEGL  SRFNKL RVVV  ADDGSEAPER
61  PVNGAHPTLQ  ADDDSLDDQD  LPLTNSQLSL  KVDSCDNCSK  QREILKQ RKV  KARLTIAAVL
121 YLLFMIGELV  GGYIANSLAI  MTDALHMLTD  LSAILITLLA  LWLSSKSPTK  RFTFGFHRLE
181 VLSAMISVLL  VYILMGFLLY  EAVQRTIHMN  YEINGDIMLI  TAAVGVA VNV  IMGFLLNQSG
241 HRHSHSHSLP  SNSPTRGSGC  ERNHGQDSL A  VRAAFVHALG  DLVQSVGVLI  AAYIIRFKPE
301 YKIADPICTY  VFSLLVAF TT  FRIIWDTVVI  ILEGVP SHLN  VDYIKEALMK  IEDVYSVEDL
361 NIWSLTSGKS  TAIVHIQLIP  GSSSKWEEVQ  SKANHLLLNT  FGMYRCTIQL  QSYRQEVDR T
421 CANCQSSSP*

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Figure 4:

Figure 4A Nucleic acid sequence alignment of the 3 variants of 108P5H8. (SEQ ID NO: 2573). Highlighted in yellow and underlined are the variations between the variants. The ORF extends from nucleotides 253-1542 of 108P5H8 v.1.

1	15	16	30	31	45	46	60	61	75	76	90
	CGGGCCCTCCAGCAG	CGGGCGCGCGGGCG	CGAGCACGACCCAC	TCTCTGCGCGCG	GGTGAGCAGCGGA	CCCCGCCCTCGTGAG					
V.1	CGGGCCCTCCAGCAG	CGGGCGCGCGGGCG	CGAGCACGACCCAC	TCTCTGCGCGCG	GGTGAGCAGCGGA	CCCCGCCCTCGTGAG					
V.2	CGGGCCCTCCAGCAG	CGGGCGCGCGGGCG	CGAGCACGACCCAC	TCTCTGCGCGCG	GGTGAGCAGCGGA	CCCCGCCCTCGTGAG					
V.3	CGGGCCCTCCAGCAG	CGGGCGCGCGGGCG	CGAGCACGACCCAC	TCTCTGCGCGCG	GGTGAGCAGCGGA	CCCCGCCCTCGTGAG					
91	105	106	120	121	135	136	150	151	165	166	180
	CCGGCCGGGGCGGG	GAGATGAGTTGCGG	CCCGCGCAGCGCC	CAGGATGGGAGGGA	CGCGCGCACTGCC	TCGAGAACTGGCGCT					
V.1	CCGGCCGGGGCGGG	GAGATGAGTTGCGG	CCCGCGCAGCGCC	CAGGATGGGAGGGA	CGCGCGCACTGCC	TCGAGAACTGGCGCT					
V.2	CCGGCCGGGGCGGG	GAGATGAGTTGCGG	CCCGCGCAGCGCC	CAGGATGGGAGGGA	CGCGCGCACTGCC	TCGAGAACTGGCGCT					
V.3	CCGGCCGGGGCGGG	GAGATGAGTTGCGG	CCCGCGCAGCGCC	CAGGATGGGAGGGA	CGCGCGCACTGCC	TCGAGAACTGGCGCT					
181	195	196	210	211	225	226	240	241	255	256	270
	CCGTGAAGTAGGCG	CCGCCGGCGCTCCGC	CTCCCCAAGCGTT	CCGCACCGCGCGCG	TCAGCCTCTGCCATG	GCCGGCTCTGGCGCG					
V.1	CCGTGAAGTAGGCG	CCGCCGGCGCTCCGC	CTCCCCAAGCGTT	CCGCACCGCGCGCG	TCAGCCTCTGCCATG	GCCGGCTCTGGCGCG					
V.2	CCGTGAAGTAGGCG	CCGCCGGCGCTCCGC	CTCCCCAAGCGTT	CCGCACCGCGCGCG	TCAGCCTCTGCCATG	GCCGGCTCTGGCGCG					
V.3	CCGTGAAGTAGGCG	CCGCCGGCGCTCCGC	CTCCCCAAGCGTT	CCGCACCGCGCGCG	TCAGCCTCTGCCATG	GCCGGCTCTGGCGCG					
271	285	286	300	301	315	316	330	331	345	346	360
	TGGAAGCGCCTCAA	TCTATGCTAAGGAAG	GATGATGCGCGCTG	TTTTTAATGACACC	AGCGCCTTTGACTTC	TCGGATGAGCGGGG					
V.1	TGGAAGCGCCTCAA	TCTATGCTAAGGAAG	GATGATGCGCGCTG	TTTTTAATGACACC	AGCGCCTTTGACTTC	TCGGATGAGCGGGG					
V.2	TGGAAGCGCCTCAA	TCTATGCTAAGGAAG	GATGATGCGCGCTG	TTTTTAATGACACC	AGCGCCTTTGACTTC	TCGGATGAGCGGGG					
V.3	TGGAAGCGCCTCAA	TCTATGCTAAGGAAG	GATGATGCGCGCTG	TTTTTAATGACACC	AGCGCCTTTGACTTC	TCGGATGAGCGGGG					
361	375	376	390	391	405	406	420	421	435	436	450
	GACGAGGGGCTTTCT	CGGTTCAACAACTT	CGAGTTGTTGGTGGCC	GATGACGGTTCCGAA	CCCCCGGAAAGGCCT	GTTAACGGGGCGCAC					
V.1	GACGAGGGGCTTTCT	CGGTTCAACAACTT	CGAGTTGTTGGTGGCC	GATGACGGTTCCGAA	CCCCCGGAAAGGCCT	GTTAACGGGGCGCAC					
V.2	GACGAGGGGCTTTCT	CGGTTCAACAACTT	CGAGTTGTTGGTGGCC	GATGACGGTTCCGAA	CCCCCGGAAAGGCCT	GTTAACGGGGCGCAC					
V.3	GACGAGGGGCTTTCT	CGGTTCAACAACTT	CGAGTTGTTGGTGGCC	GATGACGGTTCCGAA	CCCCCGGAAAGGCCT	GTTAACGGGGCGCAC					
451	465	466	480	481	495	496	510	511	525	526	540
	CCGACCCCTCCAGGCC	GACGATGATTCCTTA	CTGGACCAAGACTTA	CCTTGACCAACAGT	CAGCTGAGTTTGAAG	GTGGACTCCTGTGAC					
V.1	CCGACCCCTCCAGGCC	GACGATGATTCCTTA	CTGGACCAAGACTTA	CCTTGACCAACAGT	CAGCTGAGTTTGAAG	GTGGACTCCTGTGAC					
V.2	CCGACCCCTCCAGGCC	GACGATGATTCCTTA	CTGGACCAAGACTTA	CCTTGACCAACAGT	CAGCTGAGTTTGAAG	GTGGACTCCTGTGAC					
V.3	CCGACCCCTCCAGGCC	GACGATGATTCCTTA	CTGGACCAAGACTTA	CCTTGACCAACAGT	CAGCTGAGTTTGAAG	GTGGACTCCTGTGAC					

541 555 556 570 571 585 586 600 601 615 616 630  
 V.1 AACTGCAGCAAAACAG AGAGAGATACTGAAG CAGAGAAAGGTGAAA GCCAGGTTGACCATT GCTGCCGTTCTGTAC TTGCTTTTTCATGATT  
 V.2 AACTGCAGCAAAACAG AGAGAGATACTGAAG CAGAGAAAGGTGAAA GCCAGGTTGACCATT GCTGCCGTTCTGTAC TTGCTTTTTCATGATT  
 V.3 AACTGCAGCAAAACAG AGAGAGATACTGAAG CAGAGAAAGGTGAAA GCCAGGTTGACCATT GCTGCCGTTCTGTAC TTGCTTTTTCATGATT  
  
 631 645 646 660 661 675 676 690 691 705 706 720  
 V.1 GGAGAACTTGTAGGT GGATACATTGCAAAAT AGCTAGCAATCATG ACAGATGCACCTTCAT ATGTTAACTGACCTA AGCGCCATCATACTC  
 V.2 GGAGAACTTGTAGGT GGATACATTGCAAAAT AGCTAGCAATCATG ACAGATGCACCTTCAT ATGTTAACTGACCTA AGCGCCATCATACTC  
 V.3 GGAGAACTTGTAGGT GGATACATTGCAAAAT AGCTAGCAATCATG ACAGATGCACCTTCAT ATGTTAACTGACCTA AGCGCCATCATACTC  
  
 721 735 736 750 751 765 766 780 781 795 796 810  
 V.1 ACCCTGCTTGTCTTG TGGCTATCATCAAAA TCACCAACCAAAAAGA TTCACCTTTGGATT CATCGCTTAGAGGTT TTGTCAGCTATGATT  
 V.2 ACCCTGCTTGTCTTG TGGCTATCATCAAAA TCACCAACCAAAAAGA TTCACCTTTGGATT CATCGCTTAGAGGTT TTGTCAGCTATGATT  
 V.3 ACCCTGCTTGTCTTG TGGCTATCATCAAAA TCACCAACCAAAAAGA TTCACCTTTGGATT CATCGCTTAGAGGTT TTGTCAGCTATGATT  
  
 811 825 826 840 841 855 856 870 871 885 886 900  
 V.1 AGTGTGCTGTTGGTG TATATACCTTATGGGA TTCTCTTATATGAA GCTGTGCAAAAGAACT ATCCATATGAACCTAT GAAATAAATGGAGAT  
 V.2 AGTGTGCTGTTGGTG TATATACCTTATGGGA TTCTCTTATATGAA GCTGTGCAAAAGAACT ATCCATATGAACCTAT GAAATAAATGGAGAT  
 V.3 AGTGTGCTGTTGGTG TATATACCTTATGGGA TTCTCTTATATGAA GCTGTGCAAAAGAACT ATCCATATGAACCTAT GAAATAAATGGAGAT  
  
 901 915 916 930 931 945 946 960 961 975 976 990  
 V.1 ATAATGCTCATCACC GCAGCTGTTGGAGTT GCAGTTAATGTAATA ATGGGGTTTCTGTTG AACCCAGTCTGGTCAC CGTCACTCCCATTC  
 V.2 ATAATGCTCATCACC GCAGCTGTTGGAGTT GCAGTTAATGTAATA ATGGGGTTTCTGTTG AACCCAGTCTGGTCAC CGTCACTCCCATTC  
 V.3 ATAATGCTCATCACC GCAGCTGTTGGAGTT GCAGTTAATGTAATA ATGGGGTTTCTGTTG AACCCAGTCTGGTCAC CGTCACTCCCATTC  
  
 991 1005 1006 1020 1021 1035 1036 1050 1051 1065 1066 1080  
 V.1 CACTCCCTGCCTTCA AATCCCTTACCAGA GGTTCCTGGTGTGAA CGTAACCATGGGCAG GATAGCCTGGCAGTG AGAGCTGCATTGTA  
 V.2 CACTCCCTGCCTTCA AATCCCTTACCAGA GGTTCCTGGTGTGAA CGTAACCATGGGCAG GATAGCCTGGCAGTG AGAGCTGCATTGTA  
 V.3 CACTCCCTGCCTTCA AATCCCTTACCAGA GGTTCCTGGTGTGAA CGTAACCATGGGCAG GATAGCCTGGCAGTG AGAGCTGCATTGTA  
  
 1081 1095 1096 1110 1111 1125 1126 1140 1141 1155 1156 1170  
 V.1 CATGCTTTGGGAGAT TTGGTACAGAGTGT GGTGCTGCTAATAGCT GCATACATCATACGA TTCAAGCCAGATAAC AAGATTGCTGACCCC  
 V.2 CATGCTTTGGGAGAT TTGGTACAGAGTGT GGTGCTGCTAATAGCT GCATACATCATACGA TTCAAGCCAGATAAC AAGATTGCTGACCCC  
 V.3 CATGCTTTGGGAGAT TTGGTACAGAGTGT GGTGCTGCTAATAGCT GCATACATCATACGA TTCAAGCCAGATAAC AAGATTGCTGACCCC  
  
 1171 1185 1186 1200 1201 1215 1216 1230 1231 1245 1246 1260

100024652 100024652

v.1 ATCTGTACATACGTA TTTTCATTACTTGTG GCTTTTACAACATTT CGAATCATATGGGAT ACAGTAGTTATAATA CTAGAAGGTGTGCCA  
v.2 ATCTGTACATACGTA TTTTCATTACTTGTG GCTTTTACAACATTT CGAATCATATGGGAT ACAGTAGTTATAATA CTAGAAGGTGTGCCA  
v.3 ATCTGTACATACGTA TTTTCATTACTTGTG GCTTTTACAACATTT CGAATCATATGGGAT ACAGTAGTTATAATA CTAGAAGGTGTGCCA

1261 1275 1276 1290 1291 1305 1306 1320 1321 1335 1336 1350  
v.1 AGCCATTGTGAATGTA GACTATATCAAAAGAA GCCTTGATGAAATA GAAGATGTATATTCA GTGGAAGATTAAAT ATCTGGTCTCTCACT  
v.2 AGCCATTGTGAATGTA GACTATATCAAAAGAA GCCTTGATGAAATA GAAGATGTATATTCA GTGGAAGATTAAAT ATCTGGTCTCTCACT  
v.3 AGCCATTGTGAATGTA GACTATATCAAAAGAA GCCTTGATGAAATA GAAGATGTATATTCA GTGGAAGATTAAAT ATCTGGTCTCTCACT

1351 1365 1366 1380 1381 1395 1396 1410 1411 1425 1426 1440  
v.1 TCAGGAAAATCTACT GCCATAGTTCACATA CAGCTAATTCCTGGA AGTTCATCTAAATGG GAGGAAGTACAGTCC AAAGCAAACCATTTA  
v.2 TCAGGAAAATCTACT GCCATAGTTCACATA CAGCTAATTCCTGGA AGTTCATCTAAATGG GAGGAAGTACAGTCC AAAGCAAACCATTTA  
v.3 TCAGGAAAATCTACT GCCATAGTTCACATA CAGCTAATTCCTGGA AGTTCATCTAAATGG GAGGAAGTACAGTCC AAAGCAAACCATTTA

1441 1455 1456 1470 1471 1485 1486 1500 1501 1515 1516 1530  
v.1 TTATTGAACACATTT GGCATGTATAGATGT ACTATTGAGCTTCAG AGTTACAGGCAAGAA GTGGACAGAACTTGT GCAAAATTGTCAGAGT  
v.2 TTATTGAACACATTT GGCATGTATAGATGT ACTATTGAGCTTCAG AGTTACAGGCAAGAA GTGGACAGAACTTGT GCAAAATTGTCAGAGT  
v.3 TTATTGAACACATTT GGCATGTATAGATGT ACTATTGAGCTTCAG AGTTACAGGCAAGAA GTGGACAGAACTTGT GCAAAATTGTCAGAGT

1531 1545 1546 1560 1561 1575 1576 1590 1591 1605 1606 1620  
v.1 TCTAGTCCCTAAATTT TATGTATT TTGGG AACTCCTG-----C GTTATTTATCCTGCA GTCACAGACTTGAGA GCAATAAATGCAAAC  
v.2 TCTAGTCCCTAAATTT TATGTATT TTGGG GACTCCTG-----C GTTATTTATCCTGCA GTCACAGACTTGAGA GCAATAAATGCAAAC  
v.3 TCTAGTCCCTAAATTT TATGTATTGTTTGTAG CAJTGCTGAATTTCAC TTTATTTATCCTGCA GTCACAGACTTGAGA GCAATAAATGCAAAC

1621 1635 1636 1650 1651 1665 1666 1680 1681 1695 1696 1710  
v.1 CTAATGAGAAAATG GAATCCCTGACAGCT GTGTCCGTATCAAGC ATCAGTCTCTCAAAC AGTTGCCCCAGCCTG ACAGTGTAGTCTCT  
v.2 CTAATGAGAAAATG GAATCCCTGACAGCT GTGTCCGTATCAAGC ATCAGTCTCTCAAAC AGTTGCCCCAGCCTG ACAGTGTAGTCTCT  
v.3 CTAATGAGAAAATG GAATCCCTGACAGCT GTGTCCGTATCAAGC ATCAGTCTCTCAAAC AGTTGCCCCAGCCTG ACAGTGTAGTCTCT

1711 1725 1726 1740 1741 1755 1756 1770 1771 1785 1786 1800  
v.1 GTTTAATGGTAAAAG GAGACTTTGCCATAA TTTTCAGATGAAGAT GTTTCCCAACACTG TTTACAGAATGAGAT GTGACTCTTACAGAT  
v.2 GTTTAATGGTAAAAG GAGACTTTGCCATAA TTTTCAGATGAAGAT GTTTCCCAACACTG TTTACAGAATGAGAT GTGACTCTTACAGAT  
v.3 GTTTAATGGTAAAAG GAGACTTTGCCATAA TTTTCAGATGAAGAT GTTTCCCAACACTG TTTACAGAATGAGAT GTGACTCTTACAGAT

1801 1815 1816 1830 1831 1845 1846 1860 1861 1875 1876 1890

10024652 0020000

v.1 ACCTCATAGAGACA ATCCAGATCATACT TCATTAACTTGACAG AGTACGTGCTCTTAA GGAAGCATCAAGAAT TCAATATTTGCATTT  
 v.2 ACCTCATAG-----  
 v.3 ACCTCATAG-----  
  
 1891 1905 1906 1920 1921 1935 1936 1950 1951 1965 1966 1980  
 v.1 AAAAATACTTTTTAA GGCCATTTTATATTA AGCCAGTGTGGAAA ACTGAATTTTTTTA TTATGTATAATAATC TCGACACCCAGCTTC  
 v.2-----  
 v.3-----  
  
 1981 1995 1996 2010 2011 2025 2026 2040 2041 2055 2056 2070  
 v.1 TGGAAATGCTGCTTT CTTTTTACAGAAAT ACTACCAACAGATT TCAGGAAGTACTAGT AGTTATCCCAAAAGT GGAATAAGCATGTAT  
 v.2-----  
 v.3-----  
  
 2071 2085 2086 2100 2101 2115 2116 2130 2131 2145 2146 2160  
 v.1 TCCTAAGTGTTCAG AAATGTTTTATTCA CACAATAGTCTTAAT GTTATTGTTATGATT ATACTTTATAAACA CCITTTCCAGATGCT  
 v.2-----  
 v.3-----  
  
 2161 2175 2176 2190 2191 2205 2206 2220 2221 2235 2236 2250  
 v.1 ACAGGGTTTTGAATC TCAAAGTTAACATTT TTCAATTTTGTAAAT CTTAGAACCATAATCT TTATTTATTGTGGTC ACTGTTATTAAATGA  
 v.2-----  
 v.3-----  
  
 2251 2265 2266 2280 2281 2295 2296 2310 2311 2325 2326 2340  
 v.1 TTTAGGAAATACTTT CAATATTATTCTGAA TGGCTGAAGTTAGTC TTAAACTCAAATTAC TATATGATGATTTAA AACAAAATAAAAGAG  
 v.2-----  
 v.3-----  
  
 2341 2355 2356 2370  
 v.1 CGAGGATGGGAAAA AAAAAAAAAAAAAA AAA 2364  
 v.2----- 1548  
 v.3----- 1557

10004650 . 00000000

**Figure 4B Amino Acid Alignment of the 3 variants of 108P5H8 (SEQ ID NOS: 2570 & 2572)**

1	15	16	30	31	45	46	60	61	75	76	90
V.1	MAGSGAWKRLKSMRL	KDAPLFLNDTSAFD	FSDEAGDEGLSRFNK	LRVVADDGSEAPER	PVNGAHTLQADDD	LLDQDLPLTNSQLSL					
V.2	MAGSGAWKRLKSMRL	KDAPLFLNDTSAFD	FSDEAGDEGLSRFNK	LRVVADDGSEAPER	PVNGAHTLQADDD	LLDQDLPLTNSQLSL					
V.3	MAGSGAWKRLKSMRL	KDAPLFLNDTSAFD	FSDEAGDEGLSRFNK	LRVVADDGSEAPER	PVNGAHTLQADDD	LLDQDLPLTNSQLSL					
91	105	106	120	121	135	136	150	151	165	166	180
V.1	KVDSDCNCSKQREIL	KQKVKAHLTIAAVL	YLLFMIGELVGGYIA	NSLAIMTDALHMLTD	LSAIIITLLALWLSS	KSPTKRFTFGFHRLE					
V.2	KVDSDCNCSKQREIL	KQKVKAHLTIAAVL	YLLFMIGELVGGYIA	NSLAIMTDALHMLTD	LSAIIITLLALWLSS	KSPTKRFTFGFHRLE					
V.3	KVDSDCNCSKQREIL	KQKVKAHLTIAAVL	YLLFMIGELVGGYIA	NSLAIMTDALHMLTD	LSAIIITLLALWLSS	KSPTKRFTFGFHRLE					
181	195	196	210	211	225	226	240	241	255	256	270
V.1	VLSAMISVLLVYILM	GFLLYEAVQRTIHMN	YEINGDIMLITAAG	VAVNVIMGFLLNQSG	HRHSHSHSLPSNSPT	RGSGCERNHGQDLSLA					
V.2	VLSAMISVLLVYILM	GFLLYEAVQRTIHMN	YEINGDIMLITAAG	VAVNVIMGFLLNQSG	HRHSHSHSLPSNSPT	RGSGCERNHGQDLSLA					
V.3	VLSAMISVLLVYILM	GFLLYEAVQRTIHMN	YEINGDIMLITAAG	VAVNVIMGFLLNQSG	HRHSHSHSLPSNSPT	RGSGCERNHGQDLSLA					
271	285	286	300	301	315	316	330	331	345	346	360
V.1	VRAAFVHALGDLVQS	VGVLIAAYIIRFKPE	YKIADPICTYVFSLL	VAFTTFRIIWDTVVI	ILEGVP SHLNVDYIK	EALMKIEDVYSVEDL					
V.2	VRAAFVHALGDLVQS	VGVLIAAYIIRFKPE	YKIADPICTYVFSLL	VAFTTFRIIWDTVVI	ILEGVP SHLNVDYIK	EALMKIEDVYSVEDL					
V.3	VRAAFVHALGDLVQS	VGVLIAAYIIRFKPE	YKIADPICTYVFSLL	VAFTTFRIIWDTVVI	ILEGVP SHLNVDYIK	EALMKIEDVYSVEDL					
361	375	376	390	391	405	406	420	421			
V.1	NIWSLTSGKSTAIVH	IQLIPGSSSKWEEVQ	SKANHLLNTFGMYR	CTIQLQSYRQEVDR	CANCQSSSP						
V.2	NIWSLTSGKSTAIVH	IQLIPGSSSKWEEVQ	SKANHLLNTFGMYR	CTIQLQSYRQEVDR	CANCQSSSP						
V.3	NIWSLTSGKSTAIVH	IQLIPGSSSKWEEVQ	SKANHLLNTFGMYR	CTIQLQSYRQEVDR	CANCQSSSP						

10004652.067000

**Figure 25: Alignment of 108P5H8 v.1 protein with members of the zinc transporter family.**

A-Alignment of 108P5H8 (SEQ ID NO:2576) with the human zinc transporter 4, i.e. gi 11432533 (SEQ ID NO: 2577)

Identities = 429/429 (100%), Positives = 429/429 (100%)

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108P5: 1   MAGSGAWKRLKSMRLRKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER 60
          MAGSGAWKRLKSMRLRKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER
Sbjct: 1   MAGSGAWKRLKSMRLRKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER 60

108P5: 61   PVNGAHPTLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL 120
          PVNGAHPTLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL
Sbjct: 61   PVNGAHPTLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL 120

108P5: 121  YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPTKRFTFGFHRLE 180
          YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPTKRFTFGFHRLE
Sbjct: 121  YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPTKRFTFGFHRLE 180

108P5: 181  VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG 240
          VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG
Sbjct: 181  VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG 240

108P5: 241  HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300
          HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE
Sbjct: 241  HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300

108P5: 301  YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
          YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPSHLNVDYIKEALMKIEDVYSVEDL
Sbjct: 301  YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPSHLNVDYIKEALMKIEDVYSVEDL 360

108P5: 361  NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNTFGMYRCTIQLQSYRQEVDR 420
          NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNTFGMYRCTIQLQSYRQEVDR
Sbjct: 361  NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNTFGMYRCTIQLQSYRQEVDR 420

108P5: 421  CANCQSSSP 429
          CANCQSSSP
Sbjct: 421  CANCQSSSP 429

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B-Alignment of 108P5H8 (SEQ ID NO: 2578) with the human zinc transporter ZNT4, i.e. gi 8134840 (SEQ ID NO: 2579)

Identities = 428/429 (99%), Positives = 429/429 (99%)

```

108P5: 1   MAGSGAWKRLKSMRLRKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER 60
          MAGSGAWKRLKSMRLRKDDAPLFLNDTSAF+FSDEAGDEGLSRFNKLRVVVADDGSEAPER
Sbjct: 1   MAGSGAWKRLKSMRLRKDDAPLFLNDTSAF+FSDEAGDEGLSRFNKLRVVVADDGSEAPER 60

108P5: 61   PVNGAHPTLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL 120
          PVNGAHPTLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL
Sbjct: 61   PVNGAHPTLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL 120

108P5: 121  YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPTKRFTFGFHRLE 180
          YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPTKRFTFGFHRLE
Sbjct: 121  YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPTKRFTFGFHRLE 180

108P5: 181  VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG 240
          VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG
Sbjct: 181  VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG 240

108P5: 241  HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300
          HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE

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Sbjct: 241 HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300

108P5: 301 YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPShLNVDIKEALMKIEDVYSVEDL 360  
YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPShLNVDIKEALMKIEDVYSVEDL

Sbjct: 301 YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPShLNVDIKEALMKIEDVYSVEDL 360

108P5: 361 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNTFGMYRCTIQLQSYRQEVDR 420  
NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNTFGMYRCTIQLQSYRQEVDR

Sbjct: 361 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNTFGMYRCTIQLQSYRQEVDR 420

108P5: 421 CANCQSSSP 429  
CANCQSSSP

Sbjct: 421 CANCQSSSP 429

C-Alignment of 108P5H8 (SEQ ID NO: 2580) with the rat zinc transporter ZNT-4,  
i.e. gi 8134837 (SEQ ID NO: 2581).

Identities = 387/430 (90%), Positives = 407/430 (94%), Gaps = 3/430 (0%)

108P5: 1 MAGSGAWKRLKSMRLRKDDAPLFLNDTSADFSDDEAGDEGLSRFNKLRVAVVADDGSEAPER 60  
MAG GAWKRLKS+LRKDDAPLFLNDTSADF DE DEGLSRFNKLRVAVVADD SEAPER

Sbjct: 1 MAGPGAWKRLKSLLRKDDAPLFLNDTSADFDFLDEVSDEGLSRFNKLRVAVVADDSEAPER 60

108P5: 61 PVNGAHP TLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQRKVKARLTIAAVL 120  
PVNGAHP LQADDDSLDQ+LPLTNSQLSLK+D CDNCSK+RE+LKQRKVK RLTIAAVL

Sbjct: 61 PVNGAHPALQADDDSLDQELPLTNSQLSLKMDPCDNCSKRRELLKQRKVKTRLTIAAVL 120

108P5: 121 YLLFMIGELVGGYIANS LAIMTDALHMLTDL SAI ILTLLALWLSSKSPTKRFTFGFHRLE 180  
YLLFMIGELVGGY+ANS LAIMTDALHMLTDL SAI ILTLLALWLSSKSPT+RFTFGFHRLE

Sbjct: 121 YLLFMIGELVGGYMANSLAIMTDALHMLTDL SAI ILTLLALWLSSKSPTRRFTFGFHRLE 180

108P5: 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQ-- 238  
VLSAMISV+LVY+LMGFLLYE+QRTIHMNYEINGD+MLITAAGVAVNVIMGFLLNQ

Sbjct: 181 VLSAMISVMLVYVLMGFLLYEAMQRTIHMNYEINGDVMLITAAGVAVNVIMGFLLNQSG 240

108P5: 239 SGHRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK 298  
H H+HSHSLPSNSP+ S +HGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK

Sbjct: 241 HHHSHSHSHSLPSNSPSMVSS-GHSHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK 299

108P5: 299 PEYKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPShLNVDIKEALMKIEDVYSVE 358  
PEYKIADPICTY+FSLLVAFTT RIIWDTVVILLEGVPShLNVDIKE+LMKIEDVYSVE

Sbjct: 300 PEYKIADPICTYIFSLVAFTTLRIIWDTVVILLEGVPShLNVDIKESLMKIEDVYSVE 359

108P5: 359 DLNIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNTFGMYRCTIQLQSYRQEV 418  
DLNIWSLTSGK+TAIVH+QLIPGSSSKWEEVQSKA HLLLNTFGMY+CT+QLQSYRQE

Sbjct: 360 DLNIWSLTSGKATAIVHMLIPGSSSKWEEVQSKAKHLLLNTFGMYKCTVQLQSYRQEAT 419

108P5: 419 RTCANCQSSS 428  
RTCANCQSSS

Sbjct: 420 RTCANCQSSS 429

**Figure 1: 108P5H8 SSH sequence of 448 nucleotides (SEQ ID: ~~2549~~)**

```

1 GATCCAGATT TCTCTGCACA CTGGACTTCG TAGAGTAAGT GTGGTAGACA AAGAGACTAC
61 ACTGCACAAC CACCAAGTAA TATCATTGCT AAGAAGACTT TGGGTCGTGT TTCTCAGCCA
121 CTCTCACAGC TTTTGTAGAC TTATTTGATT TTGAAACAAG CAGTTAGCTA AATCTATTTT
181 CCTTTTATGC ATATATGTTA ATTGGCTCAA CTTAATATGG TGTTCCTTACA GAATATGAGC
241 CCATTTGAAA TAAGGTTTTA GGCAATTTTG CTGTTGGCTC TGATTTGTAT ATAGCAAATT
301 TAAAGGTACA GAGTGTTCCT TAGATAGAAG ATTAGTTCAT TTGGTTCATT TTGTCTTTGA
361 AGCAAGCCAA GCTCATGAGC CAGTTGGTTA TTTGTCTATA ATGAACACCC ATCACTATAT
421 GCTATGTTGA GGGGAGGCAA GGCTGATC

```

**Figure 2A. The cDNA (SEQ ID. NO. : ~~2549~~) and amino acid sequence (SEQ ID. NO. : ~~2579~~) of 108P5H8 v.1. The start methionine is underlined. The open reading frame extends from nucleic acid 253-1542 including the stop codon.**

```

1 gccggcctccagcagcgggcgggcgggcgggcgagcagaccccaactctcctgcggccgcg
61 ggtggagcagcgcgagcccgctcgctgagccggcgggggcggggagatgagttgcggc
121 ccgcggcagcgcggccagcatggggagggagcgcggcactgccctcgagaactggcgct
181 ccggtgaagtaggcgcgcggccgctccgcctcccccaagccgttccgcaccgcggcgcg
1      M A G S G A W K R L K S M L R K
241 tcagcctctgccATGGCGGCTCTGGCGCGTGGAAGCGCCTCAAATCTATGCTAAGGAAG
17 D D A P L F L N D T S A F D F S D E A G
301 GATGATGCGCGCTGTTTTTAAATGACACCAGCGCCTTTGACTTCTCGGATGAGGCGGGG
37 D E G L S R F N K L R V V V A D D G S E
361 GACGAGGGGCTTTCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAA
57 A P E R P V N G A H P T L Q A D D D S L
421 GCCCCGGAAGGCCTGTTAACGGGGCGCACCCGACCCTCCAGGCCGACGATGATTCCTTA
77 L D Q D L P L T N S Q L S L K V D S C D
481 CTGGACCAAGACTTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGAC
97 N C S K Q R E I L K Q R K V K A R L T I
541 AACTGCAGCAAACAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATT
117 A A V L Y L L F M I G E L V G G Y I A N
601 GCTGCCGTTCTGTACTTGTCTTTTCATGATTGGAGAACTTGTAGGTGGATACATTGCAAAT
137 S L A I M T D A L H M L T D L S A I I L
661 AGCCTAGCAATCATGACAGATGCACTTCATATGTTAACTGACCTAAGCGCCATCATACTC
157 T L L A L W L S S K S P T K R F T F G F
721 ACCCTGCTTGCTTTGTGGCTATCATCAAAATCACCAACCAAAAGATTACCTTTGGATTT
177 H R L E V L S A M I S V L L V Y I L M G

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781 CATCGCTTAGAGGTTTTGTCAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGA  
197 F L L Y E A V Q R T I H M N Y E I N G D  
841 TTCCTCTTATATGAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGAT  
217 I M L I T A A V G V A V N V I M G F L L  
901 ATAATGCTCATCACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTG  
237 N Q S G H R H S H S H S L P S N S P T R  
961 AACCAGTCTGGTCACCGTCACTCCCATTCCCCTCCCTGCCTTCAAATCCCCCTACCAGA  
257 G S G C E R N H G Q D S L A V R A A F V  
1021 GGTTCTGGGTGTGAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTGTGA  
277 H A L G D L V Q S V G V L I A A Y I I R  
1081 CATGCTTTGGGAGATTGTTGTTACAGAGTGTGTTGGTGTGCTAATAGCTGCATACATCATA  
297 F K P E Y K I A D P I C T Y V F S L L V  
1141 TTCAAGCCAGAATACAAGATTGCTGACCCCATCTGTACATACGTATTTTCATTACTTGTG  
317 A F T T F R I I W D T V V I I L E G V P  
1201 GCTTTTACAACATTTTGAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCA  
337 S H L N V D Y I K E A L M K I E D V Y S  
1261 AGCCATTTGAATGTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCA  
357 V E D L N I W S L T S G K S T A I V H I  
1321 GTCGAAGATTTAAATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATA  
377 Q L I P G S S S K W E E V Q S K A N H L  
1381 CAGCTAATTCCTGGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTTA  
397 L L N T F G M Y R C T I Q L Q S Y R Q E  
1441 TTATTGAACACATTTGGCATGTATAGATGTACTATTTCAGCTTCAGAGTTACAGGCAAGAA  
417 V D R T C A N C Q S S S P \*  
1501 GTGGACAGAACTTGTGCAAATTGTCAGAGTTCTAGTCCCTAAAttttatgtattttgggaa  
1561 ctccctgccttattttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatga  
1621 gaaaatggaatccctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccc  
1681 cagcctgacagtgctagtcctctgttttaattggtaaaaggagactttgccataattttcaga  
1741 tgaagatgtttcccaaactgtttacagaatgagatgtgactctacagatacctcatag  
1801 aagacaatccaagatcatacttcattaacttgacagagtagctgtcttaaaggaagcatc  
1861 aagaattcaatattttgcatttaaaaaataactttttaaggccattttatattaagccagtgc  
1921 tggaaaactgaattttttttattatgtataataatctcgacaccagcttctggaattgc  
1981 tgctttctttttacagaaattactaccaacagatttcaggaagtactagtagttatccc  
2041 aaaagtggaataagcatgtattcctaagtgtttcagaaatgttttatttcacacataagt  
2101 cttaatgttattgttatgattatactttataaacaaccttttcagatgctacagggttt  
2161 tgaatctcaaaggttaacattttttcattatttgaatcttagaaccaaatctttattttatt  
2221 gtgggtcactgttattaaatgatttaggaaatactttcaatattattctgaatggctgaag

~~City Docket: 511582002500~~

2281 ttagtcttaaactcaaattactatatgatgatttaaacaataaaaagagcgaggatgg  
2341 ggaaaaaaaaaaaaaaaaaaaaa

Figure 2B. The cDNA (SEQ ID. NO. :257) and amino acid sequence (SEQ ID. NO. :257) of 108P5H8 v.2. The start methionine is underlined. The open reading frame extends from nucleic acid 1-1290 including the stop codon.

```
1 M A G S G A W K R L K S M L R K D D A P
1 ATGGCCGGCTCTGGCGCGTGGGAAGCGCCTCAAATCTATGCTAAGGAAGGATGATGCGCCG
21 L F L N D T S A F D F S D E A G D E G L
61 CTGTTTTTAAATGACACCAGCGCCTTTGACTTCTCGGATGAGGCGGGGACGAGGGGCTT
41 S R F N K L R V V V A D D G S E A P E R
121 TCTCGGTTCAACAAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAAGCCCCGGAAGG
61 P V N G A H P T L Q A D D D S L L D Q D
181 CCTGTTAACGGGGCGCACCCGACCCTCCAGGCCGACGATGATTCCTTACTGGACCAAGAC
81 L P L T N S Q L S L K V D S C D N C S K
241 TTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGACAACTGCAGCAA
101 Q R E I L K Q R K V K A R L T I A A V L
301 CAGAGAGAGATACTGAAGCAGAGAAAAGGTGAAAGCCAGGTTGACCATTGCTGCCGTTCTG
121 Y L L F M I G E L V G G Y I A N S L A I
361 TACTTGCTTTTCATGATTGGAGAAGCTTGATAGGTGGATACATTGCAAATAGCCTAGCAATC
141 M T D A L H M L T D L S A I I L T L L A
421 ATGACAGATGCACTTCATATGTAACTGACCTAAGCGCCATCATACTCACCTGCTTGCT
161 L W L S S K S P T K R F T F G F H R L E
481 TTGTGGCTATCATCAAAATCACCAACCAAAAGATTACCTTTGGATTTCATCGCTTAGAG
181 V L S A M I S V L L V Y I L M G F L L Y
541 GTTTTGTCAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGATTCCTCTTATAT
201 E A V Q R T I H M N Y E I N G D I M L I
601 GAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGATATAATGCTCATC
221 T A A V G V A V N V I M G F L L N Q S G
661 ACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTGAACCACTCTGGT
241 H R H S H S H S L P S N S P T R G S G C
721 CACCGTCACTCCCATTCCCCTCCCTGCCTTCAAATCCCCTACCAGAGGTTCTGGGTGT
261 E R N H G Q D S L A V R A A F V H A L G
781 GAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTTGTACATGCTTTGGGA
281 D L V Q S V G V L I A A Y I I R F K P E
841 GATTTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGATTCAAGCCAGAA
301 Y K I A D P I C T Y V F S L L V A F T T
901 TACAAGATTGCTGATCCCATCTGTACATACGTATTTTCATTACTTGTGGCTTTTACAACA
321 F R I I W D T V V I I L E G V P S H L N
```

961 TTTCTGAATCATATGGGATACAGTAGTTATAATACTAGAAAGGTGTGCCAAGCCATTGAAT  
341 V D Y I K E A L M K I E D V Y S V E D L  
1021 GTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCAGTCGAAGATTTA  
361 N I W S L T S G K S T A I V H I Q L I P  
1081 AATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATACAGCTAATTCCT  
381 G S S S K W E E V Q S K A N H L L L N T  
1141 GGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTATTATTGAACACA  
401 F G M Y R C T I Q L Q S Y R Q E V D R T  
1201 TTTGGCATGTATAGATGTACTATTTCAGCTTCAGAGTTACAGGCAAGAAGTGGACAGAACT  
421 C A N C Q S S S P \*  
1261 TGTGCAAATTGTCAGAGTTCTAGTCCCTAAAttttatgtattttggggactcctgccttat  
1321 ttatcctgcagtcacagacttgagagcaataaatgcaaaccctaaatgagaaaatggaatc  
1381 cctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccccagcctgacagt  
1441 gctagtctctgtttaatggtaaaaggagactttgccataattttcagatgaagatgtttc  
1501 ccaaacactgtttacagaatgagatgtgactctacagatacctcatag

Figure 2C. The cDNA (SEQ ID. NO. :~~2573~~) and amino acid sequence (SEQ ID. NO. :~~2574~~) of 108P5H8 v.3. The start methionine is underlined. The open reading frame extends from nucleic acid 1-1290 including the stop codon.

```
1 M A G S G A W K R L K S M L R K D D A P
1 ATGGCCGGCTCTGGCGCGTGGAAGCGCCTCAAATCTATGCTAAGGAAGGATGATGCGCCG
21 L F L N D T S A F E F S D E A G D E G L
61 CTGTTTTTAAATGACACCAGCGCCTTTGAGTTCTCGGATGAGGCGGGGGACGAGGGGCTT
41 S R F N K L R V V V A D D G S E A P E R
121 TCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAAGCCCCGAAAGG
61 P V N G A H P T L Q A D D D S L L D Q D
181 CCTGTTAACGGGGCGCACCCGACCCTCCAGGCCGACGATGATTCCTTACTGGACCAAGAC
81 L P L T N S Q L S L K V D S C D N C S K
241 TTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGACAACTGCAGCAAA
101 Q R E I L K Q R K V K A R L T I A A V L
301 CAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATTGCTGCCGTTCTG
121 Y L L F M I G E L V G G Y I A N S L A I
361 TACTTGCTTTTCATGATTGGAGAACTTGTAGGTGGATACATTGCAAATAGCCTAGCAATC
141 M T D A L H M L T D L S A I I L T L L A
421 ATGACAGATGCACTTCATATGTTAACTGACCTAAGCGCCATCATACTCACCCCTGCTTGCT
161 L W L S S K S P T K R F T F G F H R L E
481 TTGTGGCTATCATCAAAATCACCAACCAAAAGATTACCTTTGGATTTCATCGCTTAGAG
181 V L S A M I S V L L V Y I L M G F L L Y
541 GTTTTGTCAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGATTCCTCTTATAT
201 E A V Q R T I H M N Y E I N G D I M L I
601 GAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGATATAATGCTCATC
221 T A A V G V A V N V I M G F L L N Q S G
661 ACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTGAACCAGTCTGGT
241 H R H S H S H S L P S N S P T R G S G C
721 CACCGTCACTCCCATTCCCCTCCCTGCCTTCAAATTCCCCTACCAGAGGTTCTGGGTGT
261 E R N H G Q D S L A V R A A F V H A L G
781 GAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTTGTACATGCTTTGGGA
281 D L V Q S V G V L I A A Y I I R F K P E
841 GATCTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGATTCAAGCCAGAA
301 Y K I A D P I C T Y V F S L L V A F T T
901 TACAAGATTGCTGACCCCATCTGTACATACGTATTTTCATTACTTGTGGCTTTTACAACA
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321 F R I I W D T V V I I L E G V P S H L N  
961 TTTGGAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCAAGCCATTTGAAT  
341 V D Y I K E A L M K I E D V Y S V E D L  
1021 GTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCAGTCGAAGATTTA  
361 N I W S L T S G K S T A I V H I Q L I P  
1081 AATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATACAGCTAATTCCT  
381 G S S S K W E E V Q S K A N H L L L N T  
1141 GGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTTATTATTGAACACA  
401 F G M Y R C T I Q L Q S Y R Q E V D R T  
1201 TTTGGCATGTATAGATGTACTATTCAGCTTCAGAGTTACAGGCAAGAAGTGGACAGAACT  
421 C A N C Q S S S P \*  
1261 TGTGCAAATTGTCAGAGTTCTAGTCCCTAAttttatgtattgttttagcattgctgaatt  
1321 cactttatttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatgagaaa  
1381 atggaatccctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccccagc  
1441 ctgacagtgctagtctctgtttaatggtaaaaggagactttgccataattttcagatgaa  
1501 gatgtttcccaaactgtttacagaatgagatgtgactcctacagatacctcatag

**Figure 3:**

(SEQ ID NO 2570)

**Figure 3A. Amino acid sequence corresponding to 108P5H8 v.1 and 108P5H8 v.2 (SEQ ID. NO. 2572).** The 108P5H8 v.1 and 108P5H8 v.2 proteins have 429 amino acids.

```

1  MAGSGAWKRL  KSMRLRKDDAP  LFLNDTSAFD  FSDEAGDEGL  SRFNKLRRVVV  ADDGSEAPER
61  PVNGAHPTLQ  ADDDSLDDQD  LPLTNSQLSL  KVDSCDNCSK  QREILKQRKV  KARLTIAAVL
121 YLLFMIGELV  GGYIANSLAI  MTDALHMLTD  LSAILTLTLL  LWLSSKSPTK  RFTFGFHRLE
181 VLSAMISVLL  VYILMGFLLY  EAVQRTIHMN  YEINGDIMLI  TAAVGVAENV  IMGFLLNQSG
241 HRHSHSHSLP  SNSPTRGSGC  ERNHGQDSL  A  VRAAFVHALG  DLVQSVGVLI  AAYIIRFKPE
301 YKIADPICTY  VFSLLVAFTT  FRIIWDTVVI  ILEGVPSHLN  VDYIKEALMK  IEDVYSVEDL
361 NIWSLTSGKS  TAIVHIQLIP  GSSSKWEEVQ  SKANHLLLNT  FGMYRCTIQL  QSYRQEVDR
421  CANCQSSSP*

```

**Figure 3B. Amino acid sequence corresponding to 108P5H8 v.3 (SEQ ID. NO. 2574).**  
The 108P5H8 v.3 protein has 429 amino acids.

```

1  MAGSGAWKRL  KSMRLRKDDAP  LFLNDTSAFE  FSDEAGDEGL  SRFNKLRRVVV  ADDGSEAPER
61  PVNGAHPTLQ  ADDDSLDDQD  LPLTNSQLSL  KVDSCDNCSK  QREILKQRKV  KARLTIAAVL
121 YLLFMIGELV  GGYIANSLAI  MTDALHMLTD  LSAILTLTLL  LWLSSKSPTK  RFTFGFHRLE
181 VLSAMISVLL  VYILMGFLLY  EAVQRTIHMN  YEINGDIMLI  TAAVGVAENV  IMGFLLNQSG
241 HRHSHSHSLP  SNSPTRGSGC  ERNHGQDSL  A  VRAAFVHALG  DLVQSVGVLI  AAYIIRFKPE
301 YKIADPICTY  VFSLLVAFTT  FRIIWDTVVI  ILEGVPSHLN  VDYIKEALMK  IEDVYSVEDL
361 NIWSLTSGKS  TAIVHIQLIP  GSSSKWEEVQ  SKANHLLLNT  FGMYRCTIQL  QSYRQEVDR
421  CANCQSSSP*

```

Figure 4:

(SEQ ID NO: 2573)

**Figure 4A** Nucleic acid sequence alignment of the 3 variants of 108P5H8A. Highlighted in yellow and underlined are the variations between the variants. The ORF extends from nucleotides 253-1542 of 108P5H8 v.1.

1	15	16	30	31	45	46	60	61	75	76	
90											
	v.1 GCGGCGCTCCAGCAG CCGGCGCGCGGGCG CGAGCAGACCCAC TCTCCTGCGGCGCG GGTGGAGCAGCGCGA										
	GCGGCGCTCGCTGAG										
	v.2 -----										
	-----										
	v.3 -----										
	-----										
180	91	105	106	120	121	135	136	150	151	165	166
	v.1 CCGGCGCGGGCGGG GAGATGAGTTGCGGC CCGGCGCAGCGCCC CAGGATGGGAGGGA CGCGCGCACTGCC										
	TCGAGAACTGGCGT										
	v.2 -----										
	-----										
	v.3 -----										
	-----										
270	181	195	196	210	211	225	226	240	241	255	256
	v.1 CCGGTGAAGTAGCG CCGCGCGCGCTCCGC CTCCCCAAGCCGTT CCGCACCGCGGCGC TCAGCCTCTGCCATG										
	GCGGCTCTGGCGCG										
	v.2 -----ATG										
	GCGGCTCTGGCGCG										
	v.3 -----ATG										
	GCGGCTCTGGCGCG										



271 285 286 300 301 315 316 330 331 345 346

360

V.1 TGAAGCGCCTCAAA TCTATGCTAAGGAAG GATGATGGCCGCTG TTTTAAATGACACC AGGCGCTTTGACTTC  
TCGGATGAGCGGGG  
V.2 TGAAGCGCCTCAAA TCTATGCTAAGGAAG GATGATGGCCGCTG TTTTAAATGACACC AGGCGCTTTGACTTC  
TCGGATGAGCGGGG  
V.3 TGAAGCGCCTCAAA TCTATGCTAAGGAAG GATGATGGCCGCTG TTTTAAATGACACC AGGCGCTTTGACTTC  
TCGGATGAGCGGGG

361 375 376 390 391 405 406 420 421 435 436

450

V.1 GACGAGGGGCTTTCT CGGTTCAACAACTT CGAGTTGTGTGGCC GATGACGGTTCCGAA GCCCGGAAAGGCCT  
GTTAACGGGGCGCAC  
V.2 GACGAGGGGCTTTCT CGGTTCAACAACTT CGAGTTGTGTGGCC GATGACGGTTCCGAA GCCCGGAAAGGCCT  
GTTAACGGGGCGCAC  
V.3 GACGAGGGGCTTTCT CGGTTCAACAACTT CGAGTTGTGTGGCC GATGACGGTTCCGAA GCCCGGAAAGGCCT  
GTTAACGGGGCGCAC

451 465 466 480 481 495 496 510 511 525 526

540

V.1 CCGACCCCTCCAGGCC GACGATGATTCCTTA CTGGACCAAGACTTA CCTTTGACCAACAGT CAGCTGAGTTTGAAG  
GTGGACTCCTGTGAC  
V.2 CCGACCCCTCCAGGCC GACGATGATTCCTTA CTGGACCAAGACTTA CCTTTGACCAACAGT CAGCTGAGTTTGAAG  
GTGGACTCCTGTGAC  
V.3 CCGACCCCTCCAGGCC GACGATGATTCCTTA CTGGACCAAGACTTA CCTTTGACCAACAGT CAGCTGAGTTTGAAG  
GTGGACTCCTGTGAC

541 555 556 570 571 585 586 600 601 615 616

630

V.1 AACTGCAGCAACAG AGAGAGATACTGAAG CAGAGAAAGGTGAAA GCCAGTTGACCAATT GCTGCCGTTCTGTAC  
TTGCTTTTCATGATT

V.2 AACTGCAGCAAACAG AGAGAGATACTGAAG CAGAGAAAGGTGAAA GCCAGGTTGACCATT GCTGCCGTTCTGTAC  
TTGCTTTTCATGATT  
V.3 AACTGCAGCAAACAG AGAGAGATACTGAAG CAGAGAAAGGTGAAA GCCAGGTTGACCATT GCTGCCGTTCTGTAC  
TTGCTTTTCATGATT

631 645 646 660 661 675 676 690 691 705 706

720 V.1 GGAGAACTTGTAGGT GGATACATTGCAAAAT AGCCTAGCAATCATG ACAGATGCACCTTCAT ATGTTAACTGACCCTA  
AGCGCCATCATACTC  
V.2 GGAGAACTTGTAGGT GGATACATTGCAAAAT AGCCTAGCAATCATG ACAGATGCACCTTCAT ATGTTAACTGACCCTA  
AGCGCCATCATACTC  
V.3 GGAGAACTTGTAGGT GGATACATTGCAAAAT AGCCTAGCAATCATG ACAGATGCACCTTCAT ATGTTAACTGACCCTA  
AGCGCCATCATACTC

721 735 736 750 751 765 766 780 781 795 796

810 V.1 ACCCTGCTTGCTTTG TGGCTATCATCAAAA TCACCAACCAAAAAGA TTCACCTTTGGATT CATCGCTTAGAGGTT  
TTGTCAGCTATGATT  
V.2 ACCCTGCTTGCTTTG TGGCTATCATCAAAA TCACCAACCAAAAAGA TTCACCTTTGGATT CATCGCTTAGAGGTT  
TTGTCAGCTATGATT  
V.3 ACCCTGCTTGCTTTG TGGCTATCATCAAAA TCACCAACCAAAAAGA TTCACCTTTGGATT CATCGCTTAGAGGTT  
TTGTCAGCTATGATT

811 825 826 840 841 855 856 870 871 885 886

900 V.1 AGTGTGCTGTTGGTG TATATACTTATGGGA TTCCTCTTATATGAA GCTGTGCAAAAGAACT ATCCATATGAACTAT  
GAAATAAATGGAGAT  
V.2 AGTGTGCTGTTGGTG TATATACTTATGGGA TTCCTCTTATATGAA GCTGTGCAAAAGAACT ATCCATATGAACTAT  
GAAATAAATGGAGAT  
V.3 AGTGTGCTGTTGGTG TATATACTTATGGGA TTCCTCTTATATGAA GCTGTGCAAAAGAACT ATCCATATGAACTAT  
GAAATAAATGGAGAT

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901 915 916 930 931 945 946 960 961 975 976

990

v.1 ATAATGCTCATCACC GCAGCTGTTGGAGTT GCAGTTAATGTAATA ATGGGGTTTCTGTGTTG AACCAAGCTCTGGTCAC  
CGTCACTCCCATTTCC  
v.2 ATAATGCTCATCACC GCAGCTGTTGGAGTT GCAGTTAATGTAATA ATGGGGTTTCTGTGTTG AACCAAGCTCTGGTCAC  
CGTCACTCCCATTTCC  
v.3 ATAATGCTCATCACC GCAGCTGTTGGAGTT GCAGTTAATGTAATA ATGGGGTTTCTGTGTTG AACCAAGCTCTGGTCAC  
CGTCACTCCCATTTCC

991 1005 1006 1020 1021 1035 1036 1050 1051 1065

1066

1080

v.1 CACTCCCTGCCTTCA AATTCCCCTACCAGA GGTCTGGGTGTGAA CGTAACCATGGGCAG GATAGCCTGGCAGTG  
AGAGCTGCATTTGTA  
v.2 CACTCCCTGCCTTCA AATTCCCCTACCAGA GGTCTGGGTGTGAA CGTAACCATGGGCAG GATAGCCTGGCAGTG  
AGAGCTGCATTTGTA  
v.3 CACTCCCTGCCTTCA AATTCCCCTACCAGA GGTCTGGGTGTGAA CGTAACCATGGGCAG GATAGCCTGGCAGTG  
AGAGCTGCATTTGTA

1081

1095 1096

1110 1111

1125 1126

1140 1141

1155

1156

1170

v.1 CATGCTTTGGGAGAT TTGGTACAGAGTGTT GGTGTGCTAATAGCT GCATACATCATACGA TTCAAGCCAGAATAC  
AAGATTGCTGACCCC  
v.2 CATGCTTTGGGAGAT TTGGTACAGAGTGTT GGTGTGCTAATAGCT GCATACATCATACGA TTCAAGCCAGAATAC  
AAGATTGCTGATCCC  
v.3 CATGCTTTGGGAGAT GTGGTACAGAGTGTT GGTGTGCTAATAGCT GCATACATCATACGA TTCAAGCCAGAATAC  
AAGATTGCTGACCCC

1171

1185 1186

1200 1201

1215 1216

1230 1231

1245

1246

1260

v.1 ATCTGTACATACGTA TTTTCATTACTTGTG GCTTTTACAACATTT CGAATCATATGGGAT ACAGTAGTTATAATA  
CTAGAAGGTGTGCCA

V.2 ATCTGTACATACGTA TTTTCATTACTTGTG GCTTTTACAACATTT CGAATCATATGGGAT ACAGTAGTTATAATA  
CTAGAAGGTGTGCCA

V.3 ATCTGTACATACGTA TTTTCATTACTTGTG GCTTTTACAACATTT CGAATCATATGGGAT ACAGTAGTTATAATA  
CTAGAAGGTGTGCCA

1261 1275 1276 1290 1291 1305 1306 1320 1321 1335

1336 1350

V.1 AGCCATTGGAATGTA GACTATATCAAAGAA GCCTTGATGAAAATA GAAGATGTATATTCA GTCGAAGATTTAAAT  
ATCTGGTCTCTCACT

V.2 AGCCATTGGAATGTA GACTATATCAAAGAA GCCTTGATGAAAATA GAAGATGTATATTCA GTCGAAGATTTAAAT  
ATCTGGTCTCTCACT

V.3 AGCCATTGGAATGTA GACTATATCAAAGAA GCCTTGATGAAAATA GAAGATGTATATTCA GTCGAAGATTTAAAT  
ATCTGGTCTCTCACT

1351 1365 1366 1380 1381 1395 1396 1410 1411 1425

1426 1440

V.1 TCAGGAAAATCTACT GCCATAGTTCACATA CAGCTAATTCCTGGA AGTTCAATCTAAATGG GAGGAAGTACAGTCC  
AAAGCAAACCATTTA

V.2 TCAGGAAAATCTACT GCCATAGTTCACATA CAGCTAATTCCTGGA AGTTCAATCTAAATGG GAGGAAGTACAGTCC  
AAAGCAAACCATTTA

V.3 TCAGGAAAATCTACT GCCATAGTTCACATA CAGCTAATTCCTGGA AGTTCAATCTAAATGG GAGGAAGTACAGTCC  
AAAGCAAACCATTTA

1441 1455 1456 1470 1471 1485 1486 1500 1501 1515

1516 1530

V.1 TTATTGAACACATTT GGCATGTATAGATGT ACTATTCAGCTTCAG AGTTACAGGCAAGAA GTGGACAGAACTTGT  
GCAAAATTGTCAGAGT

V.2 TTATTGAACACATTT GGCATGTATAGATGT ACTATTCAGCTTCAG AGTTACAGGCAAGAA GTGGACAGAACTTGT  
GCAAAATTGTCAGAGT

V.3 TTATTGAACACATTT GGCATGTATAGATGT ACTATTCAGCTTCAG AGTTACAGGCAAGAA GTGGACAGAACTTGT  
GCAAAATTGTCAGAGT

1531 1545 1546 1560 1561 1575 1576 1590 1591 1605  
 1606 1620  
 v.1 TCTAGTCCCTAATTT TATGTATT -TTGGG AACTCCTG-----C CTTATTATTATCCTGCA GTCACAGACTTGAGA  
 GCAATAAATGCAAAAC  
 v.2 TCTAGTCCCTAATTT TATGTATT -TTGGG GACTCCTG-----C CTTATTATTATCCTGCA GTCACAGACTTGAGA  
 GCAATAAATGCAAAAC  
 v.3 TCTAGTCCCTAATTT TATGTATTGTTTTAG CATTGCTGAATTCAC TTTATTATTATCCTGCA GTCACAGACTTGAGA  
 GCAATAAATGCAAAAC

1621 1635 1636 1650 1651 1665 1666 1680 1681 1695  
 1696 1710  
 v.1 CTAAATGAGAAAATG GAATCCCTGACAGCT GTGTCCGTATCAAGC ATCAGTCTCTCAAAC AGTTGCCCCCAGCCTG  
 ACAGTGCTAGTCTCT  
 v.2 CTAAATGAGAAAATG GAATCCCTGACAGCT GTGTCCGTATCAAGC ATCAGTCTCTCAAAC AGTTGCCCCCAGCCTG  
 ACAGTGCTAGTCTCT  
 v.3 CTAAATGAGAAAATG GAATCCCTGACAGCT GTGTCCGTATCAAGC ATCAGTCTCTCAAAC AGTTGCCCCCAGCCTG  
 ACAGTGCTAGTCTCT

1711 1725 1726 1740 1741 1755 1756 1770 1771 1785  
 1786 1800  
 v.1 GTTTAATGGTAAAG GAGACTTTGCCATAA TTTTCAGATGAAGAT GTTTCCTCCAAACACTG TTTACAGAAATGAGAT  
 GTGACTC-TACAGAT  
 v.2 GTTTAATGGTAAAG GAGACTTTGCCATAA TTTTCAGATGAAGAT GTTTCCTCCAAACACTG TTTACAGAAATGAGAT  
 GTGACTC-TACAGAT  
 v.3 GTTTAATGGTAAAG GAGACTTTGCCATAA TTTTCAGATGAAGAT GTTTCCTCCAAACACTG TTTACAGAAATGAGAT  
 GTGACTC-TACAGAT

1801 1815 1816 1830 1831 1845 1846 1860 1861 1875  
 1876 1890  
 v.1 ACCTCATAGAAGACA ATCCAAGATCATACT TCATTAACTTGACAG AGTACGTGTCTTAA GGAAGCATCAAGAAT  
 TCAATATTGCAATT

V.2 ACCTCATAG-----  
 -----  
 V.3 ACCTCATAG-----  
 -----  
 -----  
 1966 1891 1905 1906 1920 1921 1935 1936 1950 1951 1965  
 1980  
 V.1 AAAAATACTTTTAA GGCCATTTTATATTA AGCCAGTGTGAAA ACTGAATTTTTTTTA TTATGTATAATAATC  
 TCGACACCCAGCTTC  
 V.2 -----  
 -----  
 V.3 -----  
 -----  
 -----  
 2056 1981 1995 1996 2010 2011 2025 2026 2040 2041 2055  
 2070  
 V.1 TGAATGTGCTTT CTTTTACAGAAATT ACTACCCAACAGATT TCAGGAAGTACTAGT AGTTATCCCAAAAGT  
 GGAATAAGCATGTAT  
 V.2 -----  
 -----  
 V.3 -----  
 -----  
 -----  
 2146 2071 2085 2086 2100 2101 2115 2116 2130 2131 2145  
 2160  
 V.1 TCCTAAGTGTTCAG AAATGTTTTTATTCA CACATAAGTCTTAAT GTTATTGTTATGATT ATACTTTATAAACAA  
 CCTTTCCAGATGCT  
 V.2 -----  
 -----  
 V.3 -----  
 -----  
 -----

2161 2175 2176 2190 2191 2205 2206 2220 2221 2235 2236  
2250

V.1 ACAGGGTTTGAATC TCAAAGTTAACATTT TTCATTATTGTAAT CTTAGAACCAAATCT TTATTATTGTGGTC  
ACTGTTATTAAATGA

V.2 -----

V.3 -----

-----

2251 2265 2266 2280 2281 2295 2296 2310 2311 2325  
2326 2340

V.1 TTTAGGAAATACTTT CAATATTATTCTGAA TGGCTGAAGTTAGTC TTAAACTCAAATTAC TATATGATGATTAA  
AACAAAATAAAAGAG

V.2 -----

V.3 -----

-----

2341 2355 2356 2370

V.1 CGAGGATGGGAAAA AAAAAAAAAAAAAA AAA 2364

V.2 ----- 1548

V.3 ----- 1557

Figure 4B Amino Acid Alignment of the 3 variants of 108P5H8

1	15 16	30 31	45 46	60 61	75
76	90				
v.1	MAGSGAWKRLKSMRL	KDDAPLFLNDTSAFD	FSDEAGDEGLSRFNK	LRVVVADDGSEAPER	PVNGAHTLQADDD
	LLDQDLPLTNSQLSL				
v.2	MAGSGAWKRLKSMRL	KDDAPLFLNDTSAFD	FSDEAGDEGLSRFNK	LRVVVADDGSEAPER	PVNGAHTLQADDD
	LLDQDLPLTNSQLSL				
v.3	MAGSGAWKRLKSMRL	KDDAPLFLNDTSAFE	FSDEAGDEGLSRFNK	LRVVVADDGSEAPER	PVNGAHTLQADDD
	LLDQDLPLTNSQLSL				
91	105 106	120 121	135 136	150 151	165
166	180				
v.1	KVDSCDNCCKQREIL	KQKVKARLTIAAVL	YLLFMIGELVGGYIA	NSLAIMTDALHMLTD	LSAIILTLLALWLSS
	KSPTKRFTFGFHRLE				
v.2	KVDSCDNCCKQREIL	KQKVKARLTIAAVL	YLLFMIGELVGGYIA	NSLAIMTDALHMLTD	LSAIILTLLALWLSS
	KSPTKRFTFGFHRLE				
v.3	KVDSCDNCCKQREIL	KQKVKARLTIAAVL	YLLFMIGELVGGYIA	NSLAIMTDALHMLTD	LSAIILTLLALWLSS
	KSPTKRFTFGFHRLE				
181	195 196	210 211	225 226	240 241	255
256	270				
v.1	VLSAMISVLLVYILM	GFLLYEAVQRTIHMN	YEINGDIMLITAAVG	VAVNVIMGFLLNQSG	HRHSHSHSLPSNSPT
	RGSGCERNHGQDSLA				
v.2	VLSAMISVLLVYILM	GFLLYEAVQRTIHMN	YEINGDIMLITAAVG	VAVNVIMGFLLNQSG	HRHSHSHSLPSNSPT
	RGSGCERNHGQDSLA				
v.3	VLSAMISVLLVYILM	GFLLYEAVQRTIHMN	YEINGDIMLITAAVG	VAVNVIMGFLLNQSG	HRHSHSHSLPSNSPT
	RGSGCERNHGQDSLA				
271	285 286	300 301	315 316	330 331	345
346	360				



V.1 VRAAFVHALGDLVQS VGVLIAAYIIRFKPE YKIADPCTYVFSLL VAFITFRIIWDTVVI ILEGVPSHLNVDYIK  
EALMKIEDVYSVEDL  
V.2 VRAAFVHALGDLVQS VGVLIAAYIIRFKPE YKIADPCTYVFSLL VAFITFRIIWDTVVI ILEGVPSHLNVDYIK  
EALMKIEDVYSVEDL  
V.3 VRAAFVHALGDLVQS VGVLIAAYIIRFKPE YKIADPCTYVFSLL VAFITFRIIWDTVVI ILEGVPSHLNVDYIK  
EALMKIEDVYSVEDL

361	375	376	390	391	405	406	420	421	
V.1 NIWSLTSGKSTAIHV	IQLIPGSSSKWEEVQ	SKANHLLLNFTFGMYR	CTIQLQSYRQEVDR	CANCQSSSP					429
V.2 NIWSLTSGKSTAIHV	IQLIPGSSSKWEEVQ	SKANHLLLNFTFGMYR	CTIQLQSYRQEVDR	CANCQSSSP					429
V.3 NIWSLTSGKSTAIHV	IQLIPGSSSKWEEVQ	SKANHLLLNFTFGMYR	CTIQLQSYRQEVDR	CANCQSSSP					429

10024652 .062302

**Figure 25: Alignment of 108P5H8 v.1 protein with members of the zinc transporter family.**

(SEQ ID NO: 2576)

**A-Alignment of 108P5H8 with the human zinc transporter 4, i.e. gi 11432533**

(SEQ ID NO: 2577)

Identities = 429/429 (100%), Positives = 429/429 (100%)

108P5: 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER 60  
 MAGSGAWKRLKSMRLKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER  
 Sbjet: 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER 60

108P5: 61 PVNGAHPTLQADDDSLLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL 120  
 PVNGAHPTLQADDDSLLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL  
 Sbjet: 61 PVNGAHPTLQADDDSLLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL 120

108P5: 121 YLLFMIGELVGGYIANS LAIMTDALHMLTDL SAI ILTLLALWLSSKSPTKRFTFGFHRLE 180  
 YLLFMIGELVGGYIANS LAIMTDALHMLTDL SAI ILTLLALWLSSKSPTKRFTFGFHRLE  
 Sbjet: 121 YLLFMIGELVGGYIANS LAIMTDALHMLTDL SAI ILTLLALWLSSKSPTKRFTFGFHRLE 180

108P5: 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG 240  
 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG  
 Sbjet: 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG 240

108P5: 241 HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300  
 HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE  
 Sbjet: 241 HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300

108P5: 301 YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPSHLNVDYIKEALMKIEDVYSVEDL 360  
 YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPSHLNVDYIKEALMKIEDVYSVEDL  
 Sbjet: 301 YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPSHLNVDYIKEALMKIEDVYSVEDL 360

108P5: 361 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR 420  
 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR  
 Sbjet: 361 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR 420

108P5: 421 CANCQSSSP 429  
 CANCQSSSP  
 Sbjet: 421 CANCQSSSP 429

(SEQ ID NO: 2578)

**B-Alignment of 108P5H8 with the human zinc transporter ZNT4, i.e. gi 8134840**

(SEQ ID NO: 2579)

Identities = 428/429 (99%), Positives = 429/429 (99%)

108P5: 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER 60  
 MAGSGAWKRLKSMRLKDDAPLFLNDTSAF+FSDEAGDEGLSRFNKLRVVVADDGSEAPER  
 Sbjet: 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSAF+FSDEAGDEGLSRFNKLRVVVADDGSEAPER 60

108P5: 61 PVNGAHPTLQADDDSLLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL 120  
 PVNGAHPTLQADDDSLLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL  
 Sbjet: 61 PVNGAHPTLQADDDSLLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL 120

108P5: 121 YLLFMIGELVGGYIANS LAIMTDALHMLTDL SAI ILTLLALWLSSKSPTKRFTFGFHRLE 180  
 YLLFMIGELVGGYIANS LAIMTDALHMLTDL SAI ILTLLALWLSSKSPTKRFTFGFHRLE  
 Sbjet: 121 YLLFMIGELVGGYIANS LAIMTDALHMLTDL SAI ILTLLALWLSSKSPTKRFTFGFHRLE 180

108P5: 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG 240  
 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG  
 Sbjet: 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG 240

108P5: 241 HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300  
 HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE  
 Sbjet: 241 HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300

108P5: 301 YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPSHLNVDYIKEALMKIEDVYSVEDL 360  
 YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPSHLNVDYIKEALMKIEDVYSVEDL  
 Sbjct: 301 YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPSHLNVDYIKEALMKIEDVYSVEDL 360

108P5: 361 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR 420  
 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR  
 Sbjct: 361 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR 420

108P5: 421 CANCQSSSP 429  
 CANCQSSSP  
 Sbjct: 421 CANCQSSSP 429

(seq ID No: 2580)

C-Alignment of 108P5H8<sub>4</sub> with the rat zinc transporter ZNT-4, i.e. gi 8134837 (seq ID No: 2581)

Identities = 387/430 (90%), Positives = 407/430 (94%), Gaps = 3/430 (0%)

108P5: 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSADFDFDEAGDEGLSRFNKLRVVVADDGSEAPER 60  
 MAG GAWKRLKS+LRKDDAPLFLNDTSADF DE DEGLSRFNKLRVVVADD SEAPER  
 Sbjct: 1 MAGPGAWKRLKSLLRKDDAPLFLNDTSADFDFDEVSEGLSRFNKLRVVVADDSEAPER 60

108P5: 61 PVNGAHP TLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQRKVKARLTIAAVL 120  
 PVNGAHP LQADDDSLDQ+LPLTNSQLSLK+D CDNCSK+RE+LKQRKVK RL TIAAVL  
 Sbjct: 61 PVNGAHPALQADDDSLDQELPLTNSQLSLKMDPCDNCSKRRELLKQRKVKRL TIAAVL 120

108P5: 121 YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPTKRFTFGFHRLE 180  
 YLLFMIGELVGGY+ANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPT+RFTFGFHRLE  
 Sbjct: 121 YLLFMIGELVGGYMANSLAIMTDALHMLTDLSAI ILTLLALWLSSKSPTRRFTFGFHRLE 180

108P5: 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGAVNVIMGFLLNQ-- 238  
 VLSAMISV+LVY+LMGFLLYE+QRTIHMNYEINGD+MLITAAVGAVNVIMGFLLNQ  
 Sbjct: 181 VLSAMISVMLVYVLMGFLLYEAMQRTIHMNYEINGDVMLITAAVGAVNVIMGFLLNQSG 240

108P5: 239 SGHRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK 298  
 H H+HSHSLPSNSP+ S +HGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK  
 Sbjct: 241 HHHSHSHSHSLPSNSPSMVSS-GHSHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK 299

108P5: 299 PEYKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPSHLNVDYIKEALMKIEDVYSVE 358  
 PEYKIADPICTY+FSLLVAFTT RIIWDTVVILLEGVPSHLNVDYIKE+LMKIEDVYSVE  
 Sbjct: 300 PEYKIADPICTYIFSLVAFTTLRIIWDTVVILLEGVPSHLNVDYIKESLMKIEDVYSVE 359

108P5: 359 DLNIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEV 418  
 DLNIWSLTSGK+TAIVH+QLIPGSSSKWEEVQSKA HLLLNFTFGMY+CT+QLQSYRQE  
 Sbjct: 360 DLNIWSLTSGKATAIVHMLIPGSSSKWEEVQSKAKHLLLNFTFGMYKCTVQLQSYRQEAT 419

108P5: 419 RTCANCQSSS 428  
 RTCANCQSSS  
 Sbjct: 420 RTCANCQSSS 429